

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2002, 19:41:11 ; Search time 132 seconds
(without alignments)
14615.325 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 328367 seqs, 184756068 residues

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Total number of hits satisfying chosen parameters: 189310

Minimum DB seq length: 8
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Post-processing: listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	19	0.4	60	US-09-983-965-3588	Sequence 3588, Ap
4	19	0.4	63	US-09-983-965-323	Sequence 323, App
5	19	0.4	94	US-09-783-590-6963	Sequence 6963, Ap
6	19	0.4	98	US-09-969-373-1355	Sequence 1355, Ap
7	18	0.3	46	US-09-827-289-19	Sequence 19, Appl
8	18	0.3	46	US-09-827-289-23	Sequence 23, Appl
9	18	0.3	51	US-09-983-965-239	Sequence 239, App
10	18	0.3	51	US-09-948-018-31	Sequence 31, Appl
11	18	0.3	51	US-09-948-018-32	Sequence 32, Appl
12	18	0.3	59	US-09-783-590-2044	Sequence 2044, Ap
13	18	0.3	64	US-09-983-965-5341	Sequence 5341, Ap
14	18	0.3	72	US-09-919-580-221	Sequence 221, App
15	18	0.3	72	US-09-919-580-343	Sequence 343, App
16	18	0.3	72	US-09-925-300-897	Sequence 897, App
17	18	0.3	74	US-09-919-580-262	Sequence 262, App
18	18	0.3	74	US-09-919-580-394	Sequence 394, App
19	18	0.3	76	US-09-969-373-875	Sequence 875, App

c	20	18	0.3	76	10	US-09-983-965-5771	Sequence 5771, Ap
	21	18	0.3	78	10	US-09-983-965-4261	Sequence 4261, Ap
	22	18	0.3	79	10	US-09-919-580-206	Sequence 206, App
	23	18	0.3	81	10	US-09-919-580-749	Sequence 749, App
	24	18	0.3	87	10	US-09-783-590-1840	Sequence 1840, Ap
	25	18	0.3	90	10	US-09-777-564-1230	Sequence 1230, Ap
	26	18	0.3	90	10	US-09-919-580-157	Sequence 157, App
	27	18	0.3	90	10	US-09-919-580-217	Sequence 217, App
	28	18	0.3	94	10	US-09-969-373-347	Sequence 347, App
	29	18	0.3	97	10	US-09-815-343-241	Sequence 241, App
	30	18	0.3	98	10	US-09-777-564-865	Sequence 865, App
	31	18	0.3	100	10	US-09-867-701-10505	Sequence 10505, A
	32	17	0.3	17	10	US-09-788-362-3	Sequence 3, Appli
	33	17	0.3	17	10	US-09-090-672B-106	Sequence 106, App
	34	17	0.3	17	10	US-09-788-338-3	Sequence 3, Appli
c	35	17	0.3	20	10	US-09-005-243-32	Sequence 32, Appl
	36	17	0.3	20	10	US-09-005-243-33	Sequence 33, Appl
	37	17	0.3	20	10	US-09-224-683-32	Sequence 32, Appl
c	38	17	0.3	20	10	US-09-224-683-33	Sequence 33, Appl
	39	17	0.3	30	12	US-10-079-616-23	Sequence 23, Appl
	40	17	0.3	35	10	US-09-374-671-100	Sequence 100, App
	41	17	0.3	41	20	US-09-823-648-1	Sequence 1, Appli
	42	17	0.3	41	10	US-09-935-592-4	Sequence 4, Appli
c	43	17	0.3	45	10	US-09-827-289-12	Sequence 12, Appl
	44	17	0.3	45	10	US-09-827-289-16	Sequence 16, Appl
	45	17	0.3	46	10	US-09-833-498-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-016-725-4/c
; Sequence 4, Application US/10016725
; Patent No. US20020151018A1
; GENERAL INFORMATION:
; APPLICANT: Prouty, Stephen
; APPLICANT: Zhang, Lin
; APPLICANT: Stenn, Kurt
; TITLE OF INVENTION: Stearyl-CoA Desaturase Promoter
; FILE REFERENCE: J4J2065
; CURRENT APPLICATION NUMBER: US/10/016,725
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
; US-10-016-725-4

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 CGGGACCTCCACGACCGCGG 91
Db 22 CGGGACCTCCACGACCGCGG 1

RESULT 2
US-10-016-725-6/c
; Sequence 6, Application US/10016725
; Patent No. US20020151018A1
; GENERAL INFORMATION:
; APPLICANT: Prouty, Stephen
; APPLICANT: Zhang, Lin
; APPLICANT: Stenn, Kurt
; TITLE OF INVENTION: Stearyl-CoA Desaturase Promoter
; FILE REFERENCE: J4J2065
; CURRENT APPLICATION NUMBER: US/10/016,725

; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-016-725-6

Query Match 0.4%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 GCCCAGTCTGCTGCAGACGAT 262
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Db 21 GCCCAGTCTGCTGCAGACGAT 1

RESULT 3
US-09-983-965-3588/c
; Sequence 3588, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 3588
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 40-LIB3058-028-Q1-K1-B12
US-09-983-965-3588

Query Match 0.4%; Score 19; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4501 TTTTGTGCTGCTGCTGCTGCT 4519
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Db 52 TTTTGTGCTGCTGCTGCTGCT 34

RESULT 4
US-09-983-965-323/c
; Sequence 323, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678

; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 323
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 39-BOVMS1-008-Q1-E1-B4
US-09-983-965-323

Query Match 0.4%; Score 19; DB 10; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4501 TTTTGTGCTGCTGCTGCTGCT 4519
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Db 26 TTTTGTGCTGCTGCTGCTGCT 8

RESULT 5
US-09-783-590-6963
; Sequence 6963, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,201
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6963
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (83)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-6963

Query Match 0.4%; Score 19; DB 10; Length 94;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5203 ATCTAAAAAATCTAAAAA 5221
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Db 56 ATCTAAAAAATCTAAAAA 74

RESULT 6
US-09-969-373-1355
; Sequence 1355, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Eifert, Roger J.
; APPLICANT: Haug, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13

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; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1355
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1355

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Db 52 AATATATATACATATATA 70
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RESULT 7
US-09-827-289-19/c
; Sequence 19, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricia
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; FILE REFERENCE: 469390-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
US-09-827-289-19

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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5204 TCTAAAAAAAAAAAAA 5221
Db 19 TCTAAAAAAAAAAAAA 2
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RESULT 8
US-09-827-289-23/c
; Sequence 23, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricia
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
US-09-827-289-23
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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
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Db 19 TCTAAAAAAAAAAAAA 2
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RESULT 9
US-09-983-965-239/c
; Sequence 239, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 239
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 29-BOVMS1-021-Q1-E1-H9
US-09-983-965-239

Query Match          0.3%; Score 18; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4501 TTTT TTTT TTTT TTTTGGG 4518
Db 36 TTTT TTTT TTTT TTTTGGG 19
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RESULT 10
US-09-948-018-31
; Sequence 31, Application US/09948018
; Patent No. US20020150977A1
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37677
; CURRENT APPLICATION NUMBER: US/09/948,018
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 51
; TYPE: DNA
; ORGANISM: primer
US-09-948-018-31

Query Match          0.3%; Score 18; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
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Db 19 ACCACACACACACACAT 19
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US-09-919-580-343
; Sequence 343, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 57, 58, 67
; OTHER INFORMATION: n - A,T,C or G
US-09-919-580-343

Query Match 0.3%; Score 18; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4501 TTTTTTTTTTTTTTTGGG 4518
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Db 38 TTTTTTTTTTTTTTTGGG 55

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7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	39	0.7	39	17	AAT28105	Probe 10F1 isolate
3	25	0.5	51	22	AAL28163	Human SNP oligonuc
4	22	0.4	22	21	AAZ61573	Reverse PCR primer
5	22	0.4	22	24	ABL57449	Human stearyl-CoA
6	21	0.4	21	24	ABL57451	Human stearyl-CoA
7	21	0.4	21	21	AAC23240	Human secreted pro
8	21	0.4	21	24	AAI64195	Labelled probe use
9	21	0.4	95	20	AAK03761	Mouse stearyl-CoA

10	21	0.4	95	21	AAA99683	SEQ ID NO: 3 for 1
11	20	0.4	25	21	AAC96419	HLA DOA1 gene PCR
12	20	0.4	51	22	AAL32243	Human SNP oligonuc
13	20	0.4	95	17	AAT13984	Stearyl-CoA desat
14	19	0.4	21	16	AAQ75709	Reverse transcript
15	19	0.4	21	16	AAQ75609	Reverse transcript
16	19	0.4	28	24	ABK94876	Fat regulated gene
17	19	0.4	41	22	ABL40941	Human nucleotide e
18	19	0.4	51	24	AAL30447	Human SNP oligonuc
19	18	0.3	18	19	AAV54171	Nucleotide sequenc
20	18	0.3	18	21	AAZ90641	Human adipose tiss
21	18	0.3	20	16	AAQ75576	Reverse transcript
22	18	0.3	20	16	AAQ75559	Reverse transcript
23	18	0.3	21	16	AAQ75707	Reverse transcript
24	18	0.3	21	16	AAQ75710	Reverse transcript
25	18	0.3	21	16	AAQ75607	Reverse transcript
26	18	0.3	21	16	AAQ75608	Reverse transcript
27	18	0.3	21	16	AAQ75610	Reverse transcript
28	18	0.3	21	16	AAQ75628	Reverse transcript
29	18	0.3	21	16	AAQ75629	Reverse transcript
30	18	0.3	23	16	AAQ75028	Human gonadotropin
31	18	0.3	23	16	AAZ77065	Collagen IV alpha
32	18	0.3	24	24	ABL55130	Human Alport syndr
33	18	0.3	25	21	AAZ57628	Deletion sequence
34	18	0.3	25	21	AAZ48040	PCR primer GST-B2
35	18	0.3	27	20	AAZ23569	DNA EDTA probe (1-
36	18	0.3	27	20	AAZ23572	Target duplex for
37	18	0.3	29	21	AAZ47432	Human TPO anti-sen
38	18	0.3	30	19	AAV28326	Beta-globin amplic
39	18	0.3	30	22	AAH20309	NGP-polyT probe us
40	18	0.3	31	16	AAQ99580	Pseudo-loxp site B
41	18	0.3	33	20	AAZ56253	Normalised library
42	18	0.3	33	21	AAA93851	Linear probe P85 u
43	18	0.3	34	21	AAA10330	
44	18	0.3	35	16	AAQ87903	
45	18	0.3	38	18	AAT72975	

ALIGNMENTS

RESULT 1	
AAT28167/c	
ID	AAT28167 standard; DNA; 54 BP.
AC	AAZ28167;
XX	
DT	06-JAN-1997 (first entry)
XX	
DE	Senescence-related gene sequence 10F1.
XX	
KW	Human; fibroblast; AIDS; enhanced differential display; mRNA preparation;
KW	senescent cell; quiescent cell; dividing cell; senescence-related gene;
KW	gene expression; non-senescent cell; age-related lipofuscin; retina; EDD;
KW	therapy; liver spot; donor tissue; senescent melanocyte; melanin;
KW	hypopigmentation; ss.
OS	Synthetic.
XX	
PN	WO9613610-A2.
XX	
PD	09-MAY-1996.
XX	
PF	24-AUG-1995; 95WO-US11230.
XX	
PR	31-OCT-1994; 94US-0332420.
XX	
PA	(GERO-) GERON CORP.
XX	
PI	Feng J, Funk W, Hirsch KS, Linskens MHK, Villeponteau B;
PI	West MD;
XX	
DR	WPI; 1996-251464/25.

XX Identifying, isolating and regulating senescence-related genes -
PT useful to ameliorate problems associated with accumulation of
PT senescent cells, e.g. age-related lipofuscin accumulation in the
PT retina and AIDS
XX
PS Claim 8; Page 51; 135pp; English.
XX
CC AAT28076-T28113, and AAT28131-T28173 represent novel senescent-related
CC gene sequences isolated from fibroblasts using the method of the
CC invention. In the method of the invention, mRNA is isolated from a
CC senescent cell, and a young quiescent cell, and the mRNAs are amplified
CC (using primers such as those shown in AAT28044-T28075) in separate
CC reaction mixtures. The amplified sequences are then separated by size or
CC charge, and the products are analysed to identify a gene from young
CC quiescent cells and dividing cells, that is present at a different level
CC from senescent cells. To enhance the method even more, it can be
CC performed in conjunction with an enhanced differential display (EDD)
CC method (an mRNA preparation method) on the fibroblasts. The method can
CC be used for the rapid and efficient identification and isolation of
CC senescence-related genes and gene products, and to detect and distinguish
CC between senescent and non-senescent cells. It can also be used to
CC destroy cells expressing senescence specific (or related) gene products,
CC and to screen for compounds capable of altering gene expression in
CC senescent cells. The method can also be used to ameliorate problems
CC associated with the accumulation of senescent cells such as age-related
CC lipofuscin accumulation in the retina, and in the treatment of AIDS.
CC Also, the method can be used to distinguish young cells from senescent
CC cells in donor tissue, which is useful in removing senescent melanocytes
CC overexpressing melanin which cause hypopigmentation, or liver spots.
XX
SQ Sequence 54 BP; 17 A; 9 C; 9 G; 19 T; 0 other;
XX
Query Match 0.9%; Score 46; DB 17; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1410 AAAGATGATGATGTTAACCCATTCAGTACAGTATCTTTAAAT 1455
|||||
Db 46 AAAGATGATGATGTTAACCCATTCAGTACAGTATCTTTAAAT 1
XX
RESULT 2
AAT28105
ID AAT28105 standard; DNA; 39 BP.
XX
AC AAT28105;
XX
DT 31-DEC-1996 (first entry)
XX
DE Probe 10F1 isolated from fibroblasts.
XX
KW polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US11230.
XX
PR 31-OCT-1994; 94US-0332420.
XX
PA (GERO-) GERON CORP.
XX
PI Feng J, Funk W, Hirsch KS, Linskens MHK, Villeponteau B;
PI West MD;
XX

DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes -
PT useful to ameliorate problems associated with accumulation of
PT senescent cells, e.g. age-related lipofuscin accumulation in the
PT retina and AIDS
XX
PS Claim 8; Page 38; 135pp; English.
XX
CC AAT28076-T28113, and AAT28131-T28173 represent novel senescent-related
CC gene sequences isolated from fibroblasts using the method of the
CC invention. In the method of the invention, mRNA is isolated from a
CC senescent cell, and a young quiescent cell, and the mRNAs are amplified
CC (using primers such as those shown in AAT28044-T28075) in separate
CC reaction mixtures. The amplified sequences are then separated by size or
CC charge, and the products are analysed to identify a gene from young
CC quiescent cells and dividing cells, that is present at a different level
CC from senescent cells. To enhance the method even more, it can be
CC performed in conjunction with an enhanced differential display (EDD)
CC method (an mRNA preparation method) on the fibroblasts. The method can
CC be used for the rapid and efficient identification and isolation of
CC senescence-related genes and gene products, and to detect and distinguish
CC between senescent and non-senescent cells. It can also be used to
CC destroy cells expressing senescence specific (or related) gene products,
CC and to screen for compounds capable of altering gene expression in
CC senescent cells. The method can also be used to ameliorate problems
CC associated with the accumulation of senescent cells such as age-related
CC lipofuscin accumulation in the retina, and in the treatment of AIDS.
CC Also, the method can be used to distinguish young cells from senescent
CC cells in donor tissue, which is useful in removing senescent melanocytes
CC overexpressing melanin which cause hypopigmentation, or liver spots.
XX
SQ Sequence 39 BP; 11 A; 7 C; 6 G; 15 T; 0 other;
XX
Query Match 0.7%; Score 39; DB 17; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.9e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1412 AGATGATGATGTTAACCCATTCAGTACAGTATCTTTT 1450
|||||
Db 1 AGATGATGATGTTAACCCATTCAGTACAGTATCTTTT 39
XX
RESULT 3
AAL28163
ID AAL28163 standard; DNA; 51 BP.
XX
AC AAL28163;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #1371.
XX
KW immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX

PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 1772; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 51 BP; 11 A; 18 C; 15 G; 7 T; 0 other;
XX
Query Match 0.5%; Score 25; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. NO. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 200 CCCCCTGGAAGTGTATCCGGCATC 224
Db 1 CCCCCTGGAAGTGTATCCGGCATC 25
RESULT 4
AAZ61573/c
ID AAZ61573 standard; DNA: 22 BP.
XX
AC AAZ61573;
XX
DT 19-JUN-2000 (first entry)
XX
DE Reverse PCR primer used to amplify skin stearyl-CoA desaturase cDNA.
XX
KW Human; skin; stearyl-CoA desaturase; SCD; unsaturated fatty acid;
KW skin disorder; skin cancer; hypertrichosis; hirsutism; acne;
KW atopic dermatitis; alopecia; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200009754-A2.
XX
PD 24-FEB-2000.
XX
PF 12-AUG-1999; 99WO-US18387.
XX
PR 14-AUG-1998; 98US-0096520.
PR 05-AUG-1999; 99US-0096520.
XX
PA (JOHJ) JOHNSON & JOHNSON CONSUMER CO INC.
XX
PI Stenn K, Prouty SM, Parimoo S, Zhang L;
XX
DR WPI; 2000-224373/19.
XX
PT Novel nucleic acid useful for diagnosing and treating human skin
PT disorder comprises sequences encoding human stearyl-CoA desaturase -

XX
PS Disclosure; Page 46; 91pp; English.
XX
CC PCR primers AAZ61572-73 were used to amplify human skin stearyl-CoA
CC desaturase (SCD) cDNA sequences. SCD is responsible for the production
CC of unsaturated fatty acids, which are required for energy and lipid
CC metabolism, membrane structure and signal transduction. The SCD
CC polynucleotides and polypeptides are useful for diagnosing a skin
CC disorder by an abnormal level of SCD expression. The polypeptide is
CC useful for determining whether an agent increases or decreases the
CC expression level or activity of human SCD in skin cells. Such compounds
CC are useful for treating human skin disorders such as skin cancer,
CC hypertrichosis and hirsutism which is characterized by an excess of
CC SCD activity. The SCD polypeptides and polynucleotides are also useful
CC for treating human skin disorders such as acne, atopic dermatitis and
CC alopecia. The SCD polynucleotide is also useful in gene therapy.
XX
SQ Sequence 22 BP; 5 A; 8 C; 3 G; 6 T; 0 other;
XX
Query Match 0.4%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. NO. 1.8e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 861 AACTGGTGTATCCAGAGGAG 882
Db 22 AACTGGTGTATCCAGAGGAG 1
RESULT 5
ABL57449/c
ID ABL57449 standard; DNA: 22 BP.
XX
AC ABL57449;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human stearyl-CoA desaturase gene antisense PCR primer.
XX
KW Stearyl-CoA desaturase; SCD; enzyme; human; promoter; virucide;
KW dermatological; cytostatic; immunosuppressive; antiallergic;
KW antiarthritic; antiinflammatory; cardiovascular; antianaemic;
KW gene therapy; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200236780-A2.
XX
PD 10-MAY-2002.
XX
PF 31-OCT-2001; 2001WO-US45199.
XX
PR 31-OCT-2000; 2000US-244508P.
PR 30-OCT-2001; 2001US-0244508.
XX
PA (JOHJ) JOHNSON & JOHNSON CONSUMER CO INC.
XX
PI Prouty SM, Zhang L, Stenn KS;
XX
DR WPI; 2002-471502/50.
XX
PT New human stearyl-CoA desaturase gene promoter, useful for treating a
PT skin diseases (e.g. acne, psoriasis and rosacea), tumor diseases,
PT leukemias, autoimmune diseases, allergies, arthritis, inflammations, or
PT organ rejections -
XX
PS Example 2; Page 14; 53pp; English.
XX
CC The present sequence is that of a PCR primer that is complementary
CC to nucleotides -166 to -145 of the human stearyl-CoA desaturase
CC (SCD) gene (see ABL57445) on chromosome 10. The primer was used as
CC an antisense primer in the preparation of SCD-luciferase reporter
CC constructs that were used in the functional analysis of the SCD
CC promoter. The sense primers are given in ABL57446-48. The present

CC invention provides the human SCD gene promoter and its functional
CC motifs, fragments and variants, nucleic acid constructs and
CC vectors that contain such sequences, and their uses. The promoter
CC may be used for selective transgene expression in various tissues
CC such as the skin for treating a skin disease (e.g. acne, psoriasis
CC and rosacea), tumours, leukaemia, autoimmune diseases, allergy,
CC arthritis, inflammation, organ rejection, graft versus host
CC reaction, diseases of the blood coagulation system, cardiovascular
CC diseases, anaemia, infections and damage to the central nervous
CC system.
XX
SQ Sequence 22 BP; 1 A; 8 C; 10 G; 3 T; 0 other;
Query Match 0.4%; Score 22; DB 24; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 CGGGAGCTCCACGACCGCG 91
DB 22 CGGGAGCTCCACGACCGCG 1
RESULT 6
ABL57451/c
ID ABL57451 standard; DNA: 21 BP.
XX
AC ABL57451;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human stearyl-CoA desaturase gene antisense PCR primer.
XX
KW Stearyl-CoA desaturase; SCD; enzyme; human; promoter; virucide;
KW dermatological; cytostatic; immunosuppressive; antiallergic;
KW antiarthritic; antiinflammatory; cardiovascular; antianaemic;
KW gene therapy; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200236780-A2.
XX
PD 10-MAY-2002.
XX
PF 31-OCT-2001; 2001WO-US45199.
XX
PR 31-OCT-2000; 2000US-244508P.
PR 30-OCT-2001; 2001US-0244508.
XX
PA (JOHN) JOHNSON & JOHNSON CONSUMER CO INC.
XX
PI Prouty SM, Zhang L, Steen KS;
XX
DR WPI; 2002-471502/50.
XX
XX
PT New human stearyl-CoA desaturase gene promoter, useful for treating a
PT skin diseases (e.g. acne, psoriasis and rosacea), tumor diseases,
PT leukemias, autoimmune diseases, allergies, arthritis, inflammations, or
PT organ rejections -
XX
XX
PS Example 3; Page 14; 53pp; English.
XX
CC The present sequence is that of an antisense PCR primer corresponding
CC to nucleotides +7 to +27 of the human stearyl-CoA desaturase
CC (SCD) gene (see ABL57445). It was used with the sense primer given
CC in ABL57450 for the PCR amplification of an SCD gene fragment
CC (nucleotides -275 to +27) which was used in an RNase protection
CC assay to find the SCD transcription initiation site. The present
CC invention provides the human SCD gene promoter and its functional
CC motifs, fragments and variants, nucleic acid constructs and
CC vectors that contain such sequences, and their uses. The promoter
CC may be used for selective transgene expression in various tissues
CC such as the skin for treating a skin disease (e.g. acne, psoriasis
CC and rosacea), tumours, leukaemia, autoimmune diseases, allergy,

CC arthritis, inflammation, organ rejection, graft versus host
CC reaction, diseases of the blood coagulation system, cardiovascular
CC diseases, anaemia, infections and damage to the central nervous
CC system.
XX
SQ Sequence 21 BP; 4 A; 6 C; 7 G; 4 T; 0 other;
Query Match 0.4%; Score 21; DB 24; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 242 GCCCACTTGCTGCAGACGAT 262
DB 21 GCCCACTTGCTGCAGACGAT 1
RESULT 7
AAC23240
ID AAC23240 standard; CDNA: 54 BP.
XX
AC AAC23240;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 27315.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1: SEQ ID 27315; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 54 BP; 1 A; 5 C; 2 G; 46 T; 0 other;
Query Match 0.4%; Score 21; DB 21; Length 54;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2124 TTTTCTTTTCTTTTCTTT 2144


```

RESULT 10
AAA99683
ID AAA99683 standard; DNA; 95 BP.
XX
AC AAA99683;
XX
DT 06-FEB-2001 (first entry)
XX
DE .SEQ ID NO: 3 for identifying genes associated with body weight disorders.
XX
KW Mouse; body weight; immunomodulator; anorectic; obesity; cachexia;
KW thermogenesis; appetite; ds.
XX
OS Mus sp.
XX
PN US6121017-A.
XX
PD 19-SEP-2000.
XX
PF 08-OCT-1997; 97US-0946719.
XX
PR 26-FEB-1997; 97US-0807861.
PR 23-AUG-1994; 94US-0294522.
PR 06-JUN-1995; 95US-0470868.
PR 23-AUG-1995; 95US-0518878.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Tartaglia LA;
XX
DR WPI; 2000-618197/59.
XX
PT New human C5 gene and gene product, useful in regulating mammalian body
PT weight and modulating thermogenesis, especially useful for treating
PT body weight disorders, e.g. obesity or cachexia -
XX
PS Example; Fig 3B; 84pp; English.
XX
CC The present sequence shows homology to a nucleotide sequence which was
CC found to be differentially expressed in body weight disorder
CC states. The identified sequences may be useful in modulating processes
CC relating to mammalian body weight regulation, including treatment of body
CC weight disorders, e.g. obesity or cachexia, and modulation of
CC thermogenesis. It is also useful in regulating appetite and/or body
CC weight. Furthermore, it is useful for diagnostic evaluation and prognosis
CC of various body weight disorders, and for identifying subjects exhibiting
CC a predisposition to such conditions.
XX
SO Sequence 95 BP; 24 A; 24 C; 16 G; 31 T; 0 other;

Query Match 0.4%; Score 21; DB 21; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5069 TTTTTCCTTTTATGTGG 5089
    ||||||||||||||||
DB 74 TTTTTCCTTTTATGTGG 94

RESULT 11
AAC96419/C
ID AAC96419 standard; DNA; 25 BP.
XX
AC AAC96419;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #21.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX

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OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP03636.
XX
PR 26-APR-1999; 99EP-0303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences
PT of specific length -
XX
PS Claim 14; Page 51; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular.
XX
SO Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 other;

Query Match 0.4%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5202 AATCTAAAAA 5221
    ||||||||||||
DB 20 AATCTAAAAA 1

RESULT 12
AAL32243/C
ID AAL32243 standard; DNA; 51 BP.
XX
AC AAL32243;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #5451.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX

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OY 5203 ATCTAAAAAAAAAAAAAA 5221
 |||||
 Db 21 ATCTAAAAAAAAAAAAAA 3

RESULT 15

AAQ75609
 ID AAQ75609 standard; DNA; 21 BP.

XX AAQ75609;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

XX Synthetic.

OS JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes

XX PS Disclosure; Page 5; 11pp; Japanese.

XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.

XX SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 other;

Query Match 0.4%; Score 19; DB 16; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4501 TTTTGTGTGTGTGTGTGTGTGT 4519
 |||||

Db 3 TTTTGTGTGTGTGTGTGTGTGT 21

Search completed: November 14, 2002, 01:13:08
 Job time : 667 secs

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OM nucleic - nucleic search, using sw model

Run on: November 13, 2002, 23:23:31 : Search time 6984 Seconds
(without alignments)
18795.666 Million cell updates/sec

Title: US-09-918-187-3
Perfect score: 5221
Sequence: 1 ataaagggggctgagga.....aatctaaaaaaaaaaaaa 5221

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13593584

Minimum DB seq length: 8
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	1.9	98	14 US-09-021-095-3409	Sequence 3409, Ap
2	98	1.9	98	20 US-09-534-845-2201	Sequence 2201, Ap
3	98	1.9	98	20 US-09-534-845-2201	Sequence 2201, Ap
4	88	1.7	88	20 US-09-534-845-2322	Sequence 2322, Ap
5	88	1.7	88	20 US-09-534-846-2322	Sequence 2322, Ap
6	86	1.6	86	12 US-08-839-045-1181	Sequence 1181, Ap
7	86	1.6	86	20 US-09-534-845-2409	Sequence 2409, Ap
8	86	1.6	86	20 US-09-534-846-2409	Sequence 2409, Ap
9	86	1.6	86	45 US-60-015-904-1181	Sequence 1181, Ap
10	86	1.6	86	47 US-60-033-401-570	Sequence 570, App
11	81	1.6	81	17 US-09-321-214-13928	Sequence 13928, A
12	81	1.6	81	19 US-09-516-335-13928	Sequence 13928, A
13	81	1.6	81	29 US-09-733-811-13928	Sequence 13928, A
14	81	1.6	81	29 US-09-733-811A-13928	Sequence 13928, A
15	81	1.6	81	36 US-09-975-640-13928	Sequence 13928, A
16	81	1.6	81	36 US-09-975-640A-13928	Sequence 13928, A
17	80	1.5	80	20 US-09-534-845-2735	Sequence 2735, Ap
18	80	1.5	80	20 US-09-534-846-2735	Sequence 2735, Ap
19	77	1.5	77	13 US-08-940-864-94	Sequence 94, Appl
20	77	1.5	77	20 US-09-534-845-2492	Sequence 2492, Ap
21	77	1.5	77	20 US-09-534-846-2492	Sequence 2492, Ap

22	77	1.5	77	46	US-60-027-236-94	Sequence 94, Appl
23	51	1.0	51	71	US-60-278-258-1257	Sequence 1257, Ap
24	48	0.9	66	15	US-09-107-910-5087	Sequence 5087, Ap
25	48	0.9	66	20	US-09-534-845-2232	Sequence 2232, Ap
26	48	0.9	66	20	US-09-534-846-2232	Sequence 2232, Ap
27	48	0.9	88	19	US-09-522-303-403	Sequence 403, App
28	45	0.9	81	13	US-08-903-474-1413	Sequence 1413, Ap
29	45	0.9	81	20	US-09-534-845-2495	Sequence 2495, Ap
30	45	0.9	81	20	US-09-534-846-2495	Sequence 2495, Ap
31	45	0.9	81	46	US-60-023-339-5377	Sequence 5377, Ap
32	41	0.8	96	17	US-09-342-217-300	Sequence 300, App
33	41	0.8	96	17	US-09-342-217A-300	Sequence 300, App
34	41	0.8	96	34	US-09-912-293-6064	Sequence 6064, Ap
35	39	0.7	39	14	US-09-067-701-62	Sequence 62, Appl
36	35	0.7	88	20	US-09-534-845-2403	Sequence 2403, Ap
37	35	0.7	88	20	US-09-534-846-2403	Sequence 2403, Ap
38	34	0.7	51	71	US-60-278-258-1260	Sequence 1260, Ap
39	34	0.7	85	12	US-08-859-945-1680	Sequence 1680, Ap
40	34	0.7	85	20	US-09-534-845-2292	Sequence 2292, Ap
41	34	0.7	85	20	US-09-534-846-2292	Sequence 2292, Ap
42	29	0.6	94	14	US-09-075-075-1493	Sequence 1493, Ap
43	29	0.6	94	20	US-09-534-845-2490	Sequence 2490, Ap
44	29	0.6	94	20	US-09-534-846-2490	Sequence 2490, Ap
45	28	0.5	72	18	US-09-471-277-3243	Sequence 3243, Ap

ALIGNMENTS

RESULT 1

US-09-021-095-3409

Sequence 3409, Application US/09021095

GENERAL INFORMATION:

APPLICANT: Gooding, Douglas H.

APPLICANT: Stuve, Laura L.

APPLICANT: Stuart, Susan G.

APPLICANT: Ito, Laura Y.

APPLICANT: Akerblom, Ingrid E.

APPLICANT: Delegeane, Angelo M.

APPLICANT: Naughton, Rebecca E.

APPLICANT: Klingler, Tod M.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM

TITLE OF INVENTION: ADRENAL GLAND TUMOR

NUMBER OF SEQUENCES: 3656

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/021,095

FILING DATE: Herewith

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/038,210

FILING DATE: February 11, 1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: CERRONE, MICHAEL C.

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PD-0318 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 3409:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 2501485H1
US-09-021-095-3409

Query Match 1.9%; Score 98; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2918 GACGTTTCTCTTCCCTGACAGCAGCCTCCTTGTGTATTCAGAGGAGTGTAT 2977
DB 1 GACGTTTCTCTTCCCTGACAGCAGCCTCCTTGTGTATTCAGAGGAGTGTAT 60
OY 2978 GACTTGCTGTCCAGCAGCTCCCTCTGACACAGAAAT 3015
DB 61 GACTTGCTGTCCAGCAGCTCCCTCTGACACAGAAAT 98

RESULT 2

US-09-534-845-2201

Sequence 2201, Application US/09534845

GENERAL INFORMATION:

APPLICANT: Seilhamer, Jeffrey J.

APPLICANT: Delegeane, Angelo M.

APPLICANT: Stuart, Susan G.

APPLICANT: Stuve, Laura L.

APPLICANT: Mullahy, Sara J.

APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING OXIDOREDUCTASES

FILE REFERENCE: PD-1001 CIP

CURRENT APPLICATION NUMBER: US/09/534, 845

CURRENT FILING DATE: 2000-03-24

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 24058

SOFTWARE: PERL Program

SEQ ID NO 2201

LENGTH: 98

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No: hu00473404

US-09-534-845-2201

Query Match 1.9%; Score 98; DB 20; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2918 GACGTTTCTCTTCCCTGACAGCAGCCTCCTTGTGTATTCAGAGGAGTGTAT 2977
DB 1 GACGTTTCTCTTCCCTGACAGCAGCCTCCTTGTGTATTCAGAGGAGTGTAT 60
OY 2978 GACTTGCTGTCCAGCAGCTCCCTCTGACACAGAAAT 3015
DB 61 GACTTGCTGTCCAGCAGCTCCCTCTGACACAGAAAT 98

RESULT 3

US-09-534-846-2201

Sequence 2201, Application US/09534846

GENERAL INFORMATION:

APPLICANT: Seilhamer, Jeffrey J.

APPLICANT: Delegeane, Angelo M.

APPLICANT: Stuart, Susan G.

APPLICANT: Stuve, Laura L.

APPLICANT: Mullahy, Sara J.

APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING OXIDOREDUCTASES

FILE REFERENCE: PD-1001 CIP

```

; CURRENT APPLICATION NUMBER: US/09/534,846
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to file wrapper or PALM
; NUMBER OF SEQ ID NOS: 24058
; SOFTWARE: PERL Program
; SEQ ID NO 2201
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00473404
US-09-534-846-2201
```

```

Query Match          1.9%; Score 98; DB 20; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2918 GAACGTTTCTTCTTCCCTGGACAGGACCCCTTTGTGTATTGAGAGCAGTGAT 2977
DB 1 GAACGTTTCTTCTTCCCTGGACAGGACCCCTTTGTGTATTGAGAGCAGTGAT 60
QY 2978 GACTGCTGTCCAGGACGCTCCCTCTGCACACAGAAT 3015
DB 61 GACTGCTGTCCAGGACGCTCCCTCTGCACACAGAAT 98
```

```

RESULT 4
US-09-534-845-2322
; Sequence 2322, Application US/09534845
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING OXIDOREDUCTASES
; FILE REFERENCE: PD-1001 CIP
; CURRENT APPLICATION NUMBER: US/09/534,845
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 24058
; SOFTWARE: PERL Program
; SEQ ID NO 2322
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00270005
US-09-534-845-2322
```

```

Query Match          1.7%; Score 88; DB 20; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 4573 ATCTGGGTGTAATCTCTGTAAGTGTAGTCAATAGTGCATGCAAGGTTAAAAAG 4632
DB 1 ATCTGGGTGTAATCTCTGTAAGTGTAGTCAATAGTGCATGCAAGGTTAAAAAG 60
QY 4633 CGAGGTGCCCATGTATGCTGTGTTA 4660
DB 61 CGAGGTGCCCATGTATGCTGTGTTA 88
```

```

RESULT 5
US-09-534-846-2322
; Sequence 2322, Application US/09534846
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
```

```

; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING OXIDOREDUCTASES
; FILE REFERENCE: PD-1001 CIP
; CURRENT APPLICATION NUMBER: US/09/534,846
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to file wrapper or PALM
; NUMBER OF SEQ ID NOS: 24058
; SOFTWARE: PERL Program
; SEQ ID NO 2322
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00270005
US-09-534-846-2322
```

```

Query Match          1.7%; Score 88; DB 20; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 4573 ATCTGGGTGTAATCTCTGTAAGTGTAGTCAATAGTGCATGCAAGGTTAAAAAG 4632
DB 1 ATCTGGGTGTAATCTCTGTAAGTGTAGTCAATAGTGCATGCAAGGTTAAAAAG 60
QY 4633 CGAGGTGCCCATGTATGCTGTGTTA 4660
DB 61 CGAGGTGCCCATGTATGCTGTGTTA 88
```

```

RESULT 6
US-08-839-045-1181
; Sequence 1181, Application US/08839045
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akertblom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; TITLE OF INVENTION: NORMAL LUNG AND METASTATIC LUNG CARCINOMA
; NUMBER OF SEQUENCES: 1831
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,045
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/015,904
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PD-0158P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 852-0195
```

```
; INFORMATION FOR SEQ ID NO: 1181:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 86 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   IMMEDIATE SOURCE:
;   CLONE: 1238057
;   US-08-839-045-1181
```

```
Query Match          1.6%; Score 86; DB 12; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4575 CTTGGGTGTAATCTCTGTAGTGTAGCTCAAAATAGGTCATCATGAAGGTTAAAAAGCG 4634
      |||||||
Db 1 CTTGGGTGTAATCTCTGTAGTGTAGCTCAAAATAGGTCATCATGAAGGTTAAAAAGCG 60

OY 4635 AGGTGCCATGTTATGCTGTGCTTA 4660
      |||||||
Db 61 AGGTGCCATGTTATGCTGTGCTTA 86
```

```
RESULT 7
US-09-534-845-2409
; Sequence 2409, Application US/09534845
; GENERAL INFORMATION:
;   APPLICANT: Sellhauer, Jeffrey J.
;   APPLICANT: Delegeane, Angelo M.
;   APPLICANT: Stuart, Susan G.
;   APPLICANT: Stuve, Laura L.
;   APPLICANT: Mullahy, Sara J.
;   APPLICANT: Naughton, Rebecca E.
;   TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING OXIDOREDUCTASES
;   FILE REFERENCE: PD-1001 CIP
;   CURRENT APPLICATION NUMBER: US/09/534,845
;   CURRENT FILING DATE: 2000-03-24
;   Prior application data removed - refer to PALM or file wrapper
;   NUMBER OF SEQ ID NOS: 24058
;   SOFTWARE: PERL Program
;   SEQ ID NO 2409
;   LENGTH: 86
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   OTHER INFORMATION: Incyte ID No: hu00260157
;   US-09-534-845-2409
```

```
Query Match          1.6%; Score 86; DB 20; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4575 CTTGGGTGTAATCTCTGTAGTGTAGCTCAAAATAGGTCATCATGAAGGTTAAAAAGCG 4634
      |||||||
Db 1 CTTGGGTGTAATCTCTGTAGTGTAGCTCAAAATAGGTCATCATGAAGGTTAAAAAGCG 60

OY 4635 AGGTGCCATGTTATGCTGTGCTTA 4660
      |||||||
Db 61 AGGTGCCATGTTATGCTGTGCTTA 86
```

```
RESULT 8
US-09-534-846-2409
; Sequence 2409, Application US/09534846
; GENERAL INFORMATION:
;   APPLICANT: Sellhauer, Jeffrey J.
;   APPLICANT: Delegeane, Angelo M.
;   APPLICANT: Stuart, Susan G.
;   APPLICANT: Stuve, Laura L.
;   APPLICANT: Mullahy, Sara J.
;   APPLICANT: Naughton, Rebecca E.
```

```
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING OXIDOREDUCTASES
; FILE REFERENCE: PD-1001 CIP
; CURRENT APPLICATION NUMBER: US/09/534,846
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to file wrapper or PALM
; NUMBER OF SEQ ID NOS: 24058
; SOFTWARE: PERL Program
; SEQ ID NO 2409
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu00260157
;   US-09-534-846-2409
```

```
Query Match          1.6%; Score 86; DB 20; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4575 CTTGGGTGTAATCTCTGTAGTGTAGCTCAAAATAGGTCATCATGAAGGTTAAAAAGCG 4634
      |||||||
Db 1 CTTGGGTGTAATCTCTGTAGTGTAGCTCAAAATAGGTCATCATGAAGGTTAAAAAGCG 60

OY 4635 AGGTGCCATGTTATGCTGTGCTTA 4660
      |||||||
Db 61 AGGTGCCATGTTATGCTGTGCTTA 86
```

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RESULT 9
US-60-015-904-1181
; Sequence 1181, Application US/60015904
; GENERAL INFORMATION:
;   APPLICANT: Gooding, Douglas H.
;   APPLICANT: Stuve, Laura L.
;   APPLICANT: Stuart, Susan G.
;   APPLICANT: Ito, Laura Y.
;   APPLICANT: Akerblom, Ingrid E.
;   APPLICANT: Delegeane, Angelo M.
;   APPLICANT: Naughton, Rebecca E.
;   APPLICANT: Klingler, Tod M.
;   TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
;   TITLE OF INVENTION: NORMAL LUNG AND METASTATIC LUNG CARCINOMA
;   NUMBER OF SEQUENCES: 1831
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;   STREET: 3174 PORTER DRIVE
;   CITY: PALO ALTO
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/60/015,904
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: LUTHER, BARBARA J.
;   REGISTRATION NUMBER: 33954
;   REFERENCE/DOCKET NUMBER: PD-0158P
;   TELEPHONE: (415) 855-0555
;   TELEFAX: (415) 852-0195
;   INFORMATION FOR SEQ ID NO: 1181:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 86 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
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MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 1238057
US-60-015-904-1181

Query Match 1.6%; Score 86; DB 45; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4575 CTTGGGTATCTCTGTAGTGTAGCTCAATAGTCATCATGAAGCTTAAAAAGCG 4634
|||||
DB 1 CTTGGGTATCTCTGTAGTGTAGCTCAATAGTCATCATGAAGCTTAAAAAGCG 60
OY 4635 AGTGGCCATGTATGCTGTGCTTA 4660
|||||
DB 61 AGTGGCCATGTATGCTGTGCTTA 86

RESULT 10

US-60-033-401-570
; Sequence 570, Application US/60033401
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerbloom, Ingrid E.
; APPLICANT: Deleane, Angelo M.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; TITLE OF INVENTION: NEUROGANGLION TUMOR
; NUMBER OF SEQUENCES: 3552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/033,401
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0297P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 570:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; CLONE: 2306414H1
; US-60-033-401-570

Query Match 1.6%; Score 86; DB 47; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4575 CTTGGGTATCTCTGTAGTGTAGCTCAATAGTCATCATGAAGCTTAAAAAGCG 4634
|||||

DB 1 CTTGGGTATCTCTGTAGTGTAGCTCAATAGTCATCATGAAGCTTAAAAAGCG 60
OY 4635 AGTGGCCATGTATGCTGTGCTTA 4660
|||||
DB 61 AGTGGCCATGTATGCTGTGCTTA 86

RESULT 11

US-09-321-214-13928
; Sequence 13928, Application US/09321214
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Ford, John
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-740
; CURRENT APPLICATION NUMBER: US/09/321,214
; EARLIER FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: US 60/088,041
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 13928
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-321-214-13928

Query Match 1.6%; Score 81; DB 17; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4434 GCTGCTTTCTTAAGTGCACATTTGAGGAGGTGAATAATTGAATGATTTGAT 4493
|||||
DB 1 GCTGCTTTCTTAAGTGCACATTTGAGGAGGTGAATAATTGAATGATTTGAT 60
OY 4494 TTATAAGTTTTTTTTTTT 4514
|||||
DB 61 TTATAAGTTTTTTTTTTT 81

RESULT 12

US-09-516-335-13928
; Sequence 13928, Application US/09516335
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Fox, Melvin
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Jessen, Aaron
; APPLICANT: Jomek, Leni
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroza, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nelken, Sarah
; APPLICANT: Nguyen, Kody
; APPLICANT: Nguyen, Lynne

```
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Ralsi, Fariba
; APPLICANT: Randhwa, Gurpreet
; APPLICANT: Sidhu, Navjwan
; APPLICANT: Smith, Benjamin
; APPLICANT: Smythe, Ashleigh
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Wachter, Adam
; APPLICANT: Wu, James
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 740CIP
; CURRENT APPLICATION NUMBER: US/09/516,335
; EARLIER FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: 09/321,214
; EARLIER FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 60/088,041
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13928
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-516-335-13928
```

```
Query Match 1.6%; Score 81; DB 19; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 4434 GCTGCTTTCTTAAGTGCACACATTTGATGAGGCTGAAATATTGATGATTGAT 4493
DB 1 GCTGCTTTCTTAAGTGCACACATTTGATGAGGCTGAAATATTGATGATTGAT 60
OY 4494 TTATAAGTTTTTTTTTTT 4514
DB 61 TTATAAGTTTTTTTTTTT 81
```

```
RESULT 13
US-09-733-811-13928
; Sequence 13928, Application US/09733811
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandt
; APPLICANT: Fox, Melvin
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Jensen, Aaron
; APPLICANT: Jomek, Leni
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nelken, Sarah
; APPLICANT: Nguyen, Kody
; APPLICANT: Nguyen, Lynne
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Ralsi, Fariba
```

```
; APPLICANT: Randhwa, Gurpreet
; APPLICANT: Sidhu, Navjwan
; APPLICANT: Smith, Benjamin
; APPLICANT: Smythe, Ashleigh
; APPLICANT: Tkach, Joe
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 740CIP
; CURRENT APPLICATION NUMBER: US/09/733,811
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: 09/321,214
; EARLIER FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 60/088,041
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13928
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-733-811-13928
```

```
Query Match 1.6%; Score 81; DB 29; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 4434 GCTGCTTTCTTAAGTGCACACATTTGATGAGGCTGAAATATTGATGATTGAT 4493
DB 1 GCTGCTTTCTTAAGTGCACACATTTGATGAGGCTGAAATATTGATGATTGAT 60
OY 4494 TTATAAGTTTTTTTTTTT 4514
DB 61 TTATAAGTTTTTTTTTTT 81
```

```
RESULT 14
US-09-733-811A-13928
; Sequence 13928, Application US/09733811A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Ford, John
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-740
; CURRENT APPLICATION NUMBER: US/09/733,811A
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: 09/321,214
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13928
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-733-811A-13928
```

```
Query Match 1.6%; Score 81; DB 29; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 4434 GCTGCTTTCTTAAGTGCACACATTTGATGAGGCTGAAATATTGATGATTGAT 4493
DB 1 GCTGCTTTCTTAAGTGCACACATTTGATGAGGCTGAAATATTGATGATTGAT 60
OY 4494 TTATAAGTTTTTTTTTTT 4514
DB 61 TTATAAGTTTTTTTTTTT 81
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Db 61 TTATAGTTTTTTTTTTTTT 81

Job time : 7011 secs

RESULT 15
US-09-975-640-13928

; Sequence 13928, Application US/09975640
; GENERAL INFORMATION:

; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Fox, Melvin
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Jessen, Aaron
; APPLICANT: Jomek, Ienl
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nelken, Sarah
; APPLICANT: Nguyen, Kody
; APPLICANT: Nguyen, Lynne
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisl, Fariba
; APPLICANT: Randhwa, Gurpreet
; APPLICANT: Sidhu, Navjwan
; APPLICANT: Smith, Benjamin
; APPLICANT: Smythe, Ashleigh
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Wachter, Adam
; APPLICANT: Wu, James
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 740CIP
; CURRENT APPLICATION NUMBER: US/09/975,640
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/733,811
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/088,041
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13928
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-975-640-13928

Query Match 1.6%; Score 81; DB 36; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4434 GCTGCTTTCTTAAGTCCACATTTGATGAGCGGTGGAATAATTGAATGTAATTTGAT 4493
|||||
Db 1 GCTGCTTTCTTAAGTCCACATTTGATGAGCGGTGGAATAATTGAATGTAATTTGAT 60
|||||
QY 4494 TTATAAGTTTTTTTTTTTTT 4514
|||||
Db 61 TTATAAGTTTTTTTTTTTTT 81

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2002, 20:20:34 ; Search time 66 seconds
(without alignments)
13362.707 Million cell updates/sec

Title: US-09-918-187-3
Perfect score: 5221
Sequence: 1 ataaagggggtgagga.....aatctaaaaaaaaaaaaa 5221

Scoring table: OLIGO_MUC
Gapop 60.0 , Gapext 60.0

Searched: 209617 seqs, 84460702 residues

Word size : 0

Total number of hits satisfying chosen parameters: 282408

Minimum DB seq length: 8
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	0.4	54	US-09-513-999C-27315	Sequence 27315, A
2	18	0.3	44	PCT-US02-32367-19	Sequence 19, Appl
3	18	0.3	44	US-10-267-922-19	Sequence 19, Appl
4	18	0.3	52	US-09-513-999C-17952	Sequence 17952, A
5	18	0.3	61	US-09-513-999C-27797	Sequence 27797, A
6	18	0.3	67	US-09-513-999C-16021	Sequence 16021, A
7	18	0.3	69	US-09-513-999C-20419	Sequence 20419, A
8	17	0.3	22	PCT-US02-33002-9	Sequence 9, Appl
9	17	0.3	22	PCT-US02-33002-18	Sequence 18, Appl
10	17	0.3	56	US-09-513-999C-29760	Sequence 29760, A
11	17	0.3	57	US-09-513-999C-22073	Sequence 22073, A
12	17	0.3	61	US-09-513-999C-18892	Sequence 18892, A
13	17	0.3	61	US-09-513-999C-19473	Sequence 19473, A
14	17	0.3	73	US-09-513-999C-33156	Sequence 33156, A
15	17	0.3	77	US-60-416-172-130	Sequence 130, App
16	17	0.3	84	US-09-513-999C-20557	Sequence 20557, A
17	17	0.3	86	US-09-513-999C-19830	Sequence 19830, A
18	17	0.3	87	US-09-513-999C-29018	Sequence 29018, A
19	17	0.3	88	US-09-513-999C-17274	Sequence 17274, A
20	17	0.3	88	US-09-513-999C-20729	Sequence 20729, A
21	17	0.3	89	US-09-513-999C-27453	Sequence 27453, A
22	17	0.3	90	US-09-513-999C-16433	Sequence 16433, A
23	17	0.3	90	US-09-513-999C-20579	Sequence 20579, A
24	17	0.3	91	US-09-513-999C-14518	Sequence 14518, A
25	17	0.3	91	US-09-513-999C-28101	Sequence 28101, A
26	17	0.3	96	US-09-513-999C-17469	Sequence 17469, A

27	17	0.3	98	5	US-09-513-999C-23475	Sequence 23475, A
28	17	0.3	98	5	US-09-513-999C-34732	Sequence 34732, A
29	17	0.3	100	5	US-09-513-999C-16076	Sequence 16076, A
30	16	0.3	22	1	PCT-US02-33002-7	Sequence 7, Appl
31	16	0.3	22	1	PCT-US02-33002-8	Sequence 8, Appl
32	16	0.3	22	1	PCT-US02-33002-10	Sequence 10, Appl
33	16	0.3	22	1	PCT-US02-33002-15	Sequence 15, Appl
34	16	0.3	22	1	PCT-US02-33002-17	Sequence 17, Appl
35	16	0.3	22	1	PCT-US02-33002-16	Sequence 16, Appl
36	16	0.3	25	7	US-60-417-190-48907	Sequence 48907, A
37	16	0.3	25	7	US-60-417-190-48908	Sequence 48908, A
38	16	0.3	25	7	US-60-417-190-48909	Sequence 48909, A
39	16	0.3	25	7	US-60-417-190-48910	Sequence 48910, A
40	16	0.3	25	7	US-60-417-190-48911	Sequence 48911, A
41	16	0.3	25	7	US-60-417-190-48912	Sequence 48912, A
42	16	0.3	27	6	US-10-281-513-153	Sequence 153, App
43	16	0.3	32	6	US-10-281-513-245	Sequence 245, App
44	16	0.3	35	5	US-09-518-813B-60	Sequence 60, Appl
45	16	0.3	37	5	US-09-791-190-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-513-999C-27315
; Sequence 27315, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; PRIOR APPLICATION NUMBER: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 27315
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-513-999C-27315

Query Match 0.4%; Score 21; DB 5; Length 54;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2124 TTTTCTTTCTTTCTTTCTTT 2144
DB 14 TTTTCTTTCTTTCTTTCTTT 34

RESULT 2
PCT-US02-32367-19/c
; Sequence 19, Application PC/TUS0232367
; GENERAL INFORMATION:
; APPLICANT: CHIRON CORPORATION et al.
; TITLE OF INVENTION: IDENTIFICATION OF OLIGONUCLEOTIDES FOR THE CAPTURE,
; FILE REFERENCE: 2301-18346.40 / PP18346.005
; CURRENT APPLICATION NUMBER: PCT/US02/32367
; CURRENT FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide VHBV39

PCT-US02-32367-19

Query Match 0.3%; Score 18; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4498 AACGTTTTTTTTTTTTTT 4515
|||||
DB 24 AACGTTTTTTTTTTTTTT 7

RESULT 3
US-10-267-922-19/c
; Sequence 19, Application US/10267922
; GENERAL INFORMATION:
; APPLICANT: SHYAMALA, Venkatakrishna
; TITLE OF INVENTION: IDENTIFICATION OF OLIGONUCLEOTIDES FOR THE CAPTURE,
; TITLE OF INVENTION: DETECTION AND QUANTITATION OF HEPATITIS B VIRAL DNA
; FILE REFERENCE: 2301-18346 / Pp18346.004
; CURRENT APPLICATION NUMBER: US/10/267,922
; CURRENT FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-267-922-19

Query Match 0.3%; Score 18; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4498 AACGTTTTTTTTTTTTTT 4515
|||||
DB 24 AACGTTTTTTTTTTTTTT 7

RESULT 4
US-09-513-999C-17952/c
; Sequence 17952, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 17952
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-17952

Query Match 0.3%; Score 18; DB 5; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4501 TTTTGTGTGTGTGTGTGGG 4518
|||||
DB 51 TTTTGTGTGTGTGTGTGGG 34

RESULT 5
US-09-513-999C-27797

; Sequence 27797, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 27797
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-27797

Query Match 0.3%; Score 18; DB 5; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5204 TCTAATAAAAAAAAAAAAAA 5221
|||||
DB 44 TCTAATAAAAAAAAAAAAAA 61

RESULT 6
US-09-513-999C-16021
; Sequence 16021, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16021
; LENGTH: 67
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-16021

Query Match 0.3%; Score 18; DB 5; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5204 TCTAATAAAAAAAAAAAAAA 5221
|||||
DB 46 TCTAATAAAAAAAAAAAAAA 63

RESULT 7
US-09-513-999C-20419
; Sequence 20419, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm

```
; SEQ ID NO 20419
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-20419
```

```
Query Match          0.3%; Score 18; DB 5; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5204 TCTAAAAAAAAAAAAA 5221
      |||
Db 49 TCTAAAAAAAAAAAAA 66
```

RESULT 8

```
PCT-US02-33002-9/c
; Sequence 9, Application PC/TUS0233002
; GENERAL INFORMATION:
; APPLICANT: Serafini, Tito
; APPLICANT: Chen, Hang
; APPLICANT: Toemel, Emily
; APPLICANT: Ellis, Michael
; TITLE OF INVENTION: Methods for Nucleic Acid Amplification
; FILE REFERENCE: 2605-1-002PCT
; CURRENT APPLICATION NUMBER: PCT/US02/33002
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 10/036,860
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/305,666
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
PCT-US02-33002-9
```

```
Query Match          0.3%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5205 CTAATAAAAAAAAAA 5221
      |||
Db 22 CTAATAAAAAAAAAA 6
```

RESULT 9

```
PCT-US02-33002-18
; Sequence 18, Application PC/TUS0233002
; GENERAL INFORMATION:
; APPLICANT: Serafini, Tito
; APPLICANT: Chen, Hang
; APPLICANT: Toemel, Emily
; APPLICANT: Ellis, Michael
; TITLE OF INVENTION: Methods for Nucleic Acid Amplification
; FILE REFERENCE: 2605-1-002PCT
; CURRENT APPLICATION NUMBER: PCT/US02/33002
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 10/036,860
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/305,666
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: synthetic sequence
PCT-US02-33002-18
```

```
Query Match          0.3%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4501 TTTT TTTT TTTT TTTT TTTG 4517
      |||
Db 6 TTTT TTTT TTTT TTTT TTTG 22
```

RESULT 10

```
US-09-513-999C-29760
; Sequence 29760, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 29760
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-29760
```

```
Query Match          0.3%; Score 17; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5205 CTAATAAAAAAAAAA 5221
      |||
Db 38 CTAATAAAAAAAAAA 54
```

RESULT 11

```
US-09-513-999C-22073
; Sequence 22073, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 22073
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-22073
```

```
Query Match          0.3%; Score 17; DB 5; Length 57;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5205 CTAATAAAAAAAAAA 5221
      |||
Db 41 CTAATAAAAAAAAAA 57
```

RESULT 12

```
US-09-513-999C-18892/c
; Sequence 18892, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 18892
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-18892
```

```
Query Match          0.3%; Score 17; DB 5; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4501 TTTTCTTTCTTTCTTTGCG 4517
      |||||||
Db 56 TTTTCTTTCTTTCTTTGCG 40
```

```
RESULT 13
US-09-513-999C-19473
; Sequence 19473, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 19473
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-19473
```

```
Query Match          0.3%; Score 17; DB 5; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2124 TTTTCTTTCTTTCTTTT 2140
      |||||||
Db 38 TTTTCTTTCTTTCTTTT 54
```

```
RESULT 14
US-09-513-999C-33156
; Sequence 33156, Application us/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
```

```
; SOFTWARE: Patent.pm
; SEQ ID NO 33156
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-33156
```

```
Query Match          0.3%; Score 17; DB 5; Length 73;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4499 AGTTTCTTTCTTTCTTTT 4515
      |||||||
Db 52 AGTTTCTTTCTTTCTTTT 68
```

```
RESULT 15
US-60-416-172-130
; Sequence 130, Application US/60416172
; GENERAL INFORMATION:
; APPLICANT: Chang, Hwai Wen
; APPLICANT: Felts, Katherine A.
; APPLICANT: Warren, Amy J.
; APPLICANT: Cooper, Judith R.
; TITLE OF INVENTION: Genes from Human Cancer Cells and Human Tumors
; FILE REFERENCE: 216019-153
; CURRENT APPLICATION NUMBER: US/60/416,172
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 130
; LENGTH: 77
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic primer (cDNA an
; OTHER INFORMATION: r primer)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Base 1 is a biotinylated guanosine residue
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (75)..(75)
; OTHER INFORMATION: V stands for A, C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (76)..(77)
; OTHER INFORMATION: N stands for A, C, G or T
US-60-416-172-130
```

```
Query Match          0.3%; Score 17; DB 7; Length 77;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4499 AGTTTCTTTCTTTCTTTT 4515
      |||||||
Db 55 AGTTTCTTTCTTTCTTTT 71
```

Search completed: November 14, 2002, 01:20:47
Job time : 70 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 14, 2002, 01:16:55 ; Search time 4418 Seconds
(without alignments)
19139.121 Million cell updates/sec

Title: US-09-918-187-3

Perfect score: 5221

Sequence: 1 ataaagggggcgtgagga.....aatctaaaaaaaaaaaaa 5221

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 357786

Minimum DB seq length: 8
Maximum DB seq length: 100

Post-processing: listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estlin:*
 - 4: em_estlmu:*
 - 5: em_estlov:*
 - 6: em_estlpl:*
 - 7: em_estlro:*
 - 8: em_estlrc:*
 - 9: gb_estl:*
 - 10: gb_estl2:*
 - 11: gb_estl3:*
 - 12: gb_estl4:*
 - 13: gb_estl5:*
 - 14: gb_estl6:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
 - 20: em_gss_pln:*
 - 21: em_gss_vrt:*
 - 22: em_gss_fun:*
 - 23: em_gss_mam:*
 - 24: em_gss_mus:*
 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rpod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	88	1.7	91	10	BE546379	601071061
2	73	1.4	73	12	BG113100	BG113100 602283756
3	58	1.1	100	12	BE695455	BE695455 MRI-BT079
4	50	1.0	50	9	AU103573	AU103573 AU103573
5	50	1.0	50	9	AU103578	AU103578 AU103578
6	47	0.9	50	9	AU103571	AU103571 AU103571

7	43	0.8	74	12	BG255827	BG255827 602368138
8	42	0.8	42	13	BI223563	BI223563 602941991
9	40	0.8	68	9	AA501922	AA501922 n954d08.s
10	32	0.6	32	13	BI259338	BI259338 602972590
11	28	0.5	50	9	AU103576	AU103576 AU103576
12	26	0.5	50	9	AU103570	AU103570 AU103570
13	24	0.5	50	9	AU103572	AU103572 AU103572
14	24	0.5	92	9	AA544229	AA544229 vj63d12.r
15	22	0.4	68	12	BE957444	BE957444 601653588
16	21	0.4	58	12	BG244918	BG244918 602358371
17	21	0.4	66	17	AZ373877	AZ373877 1M0126005
18	21	0.4	73	9	AI223491	AI223491 qx27c06.x
19	21	0.4	94	9	AI339479	AI339479 q116d01.x
20	21	0.4	97	17	AZ431988	AZ431988 1M0217N07
21	20	0.4	37	2	HSM001541	HSM001541 Homo sapi
22	20	0.4	37	10	AV947979	AV947979 Homo sapi
23	20	0.4	38	10	AV739303	AV739303 AV739303
24	20	0.4	38	17	AZ345865	AZ345865 1M0080J15
25	20	0.4	39	10	AV949716	AV949716 AV949716
26	20	0.4	42	17	AZ625468	AZ625468 1M0464N22
27	20	0.4	47	10	AV948822	AV948822 AV948822
28	20	0.4	50	17	AZ657819	AZ657819 1M0534E17
29	20	0.4	50	17	AL771848	AL771848 Arabidops
30	20	0.4	52	9	AA611743	AA611743 v089h05.r
31	20	0.4	52	10	AW103102	AW103102 x043e05.x
32	20	0.4	53	9	AA528632	AA528632 n102f07.s
33	20	0.4	54	10	AW695135	AW695135 NF091F01S
34	20	0.4	56	9	AI401100	AI401100 t022d05.x
35	20	0.4	56	14	T25677	T25677 EST00547 Eq
36	20	0.4	58	9	AU264276	AU264276 AU264276
37	20	0.4	58	14	BQ385703	BQ385703 NISC_mn13
38	20	0.4	59	14	BQ614971	BQ614971 fab20905.
39	20	0.4	61	2	HSM001540	HSM001540 Homo sapi
40	20	0.4	61	9	AI630615	AI630615 ad13c06.x
41	20	0.4	63	2	HSM001534	HSM001534 Homo sapi
42	20	0.4	63	12	BG798256	BG798256 1c07e08.y
43	20	0.4	64	2	HSW001522	HSW001522 Homo sapi
44	20	0.4	67	9	AI348943	AI348943 cb60a11.x
45	20	0.4	68	13	BMS31526	BMS31526 fx88b07.y

ALIGNMENTS

RESULT 1
LOCUS BE546379 91 bp mRNA EST 09-AUG-2000
DEFINITION 601071061F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3457239 5',
mRNA sequence.
ACCESSION BE546379
VERSION BE546379.1 GI:9775024
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
TITLE 1 (bases 1 to 91)
JOURNAL Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
COMMENT Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNL at:
http://image.llnl.gov
Plate: L1AM8446 row: 1 column: 16
High quality sequence stop: 91.
Location/Qualifiers
1..91

FEATURES
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3457239"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

BASE COUNT      22 a      24 c      26 g      19 t
ORIGIN

Query Match      1.7%; Score 88; DB 10; Length 91;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3230 GTTGAGCCAGTGGGCCAGCCACAGACGAAAGAGGGTTTATTTTCAGTCCCTCTCTCTG 3289
      |||
Db   4 GTTGAGCCAGTGGGCCAGCCACAGACGAAAGAGGGTTTATTTTCAGTCCCTCTCTCTG 63

QY  3290 GGTCAAGACCAGAGGGCATGCTGAATGC 3317
      |||
Db   64 GGTCAAGACCAGAGGGCATGCTGAATGC 91

RESULT 2
BG13100      73 bp      mRNA      linear      EST 30-JAN-2001
LOCUS      602283756f1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4371325 5',
DEFINITION      mRNA sequence.
ACCESSION      BG13100
VERSION      BG13100.1 GI:12606606
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 73)
AUTHORS      NIH-MGC http://mgs.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1998)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-remail.nih.gov
      Tissue Procurement: ATCC
      cDNA Library Preparation: Life Technologies, Inc.
      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
      DNA Sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      http://image.llnl.gov
      Plate: LLAM10029 row: p column: 14
      High quality sequence stop: 73.
FEATURES
      source
      1..73
      location/Qualifiers
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:4371325"
      /clone_lib="NIH_MGC_86"
      /tissue_type="osteosarcoma, cell line"
      /lab_host="DH10B (phage-resistant)"
      /note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
      Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
      Average insert size 1.533 kb. Library enriched for
      full-length clones and constructed by Life Technologies.
      Note: this is a NIH-MGC library."

BASE COUNT      12 a      20 c      19 g      22 t
ORIGIN

Query Match      1.4%; Score 73; DB 12; Length 73;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY  3263 GGGTTATTTTCAGTCCCTCTCTCTGGTCAAGACGAGGGCATGCTGAATGCCCCCT 3322
      |||
Db   1 GGGTTATTTTCAGTCCCTCTCTCTGGTCAAGACGAGGGCATGCTGAATGCCCCCT 60

QY  3323 GCTTACTTGGTGA 3335
      |||
Db   61 GCTTACTTGGTGA 73

RESULT 3
BE695455
LOCUS      BE695455      100 bp      mRNA      linear      EST 11-SEP-2000
DEFINITION      MRI-BT0796-160600-001-c10 BT0796 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BE695455
VERSION      BE695455.1 GI:10082615
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 100)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
      Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
      Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
      Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
      ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
      Simpson,A.J.
      Shotgun sequencing of the human transcriptome with ORF expressed
      sequence tags
      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
      20202663
      Contact: Simpson A.J.G.
      Laboratory of Cancer Genetics
      Ludwig Institute for Cancer Research
      Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
      Brazil
      Tel: +55-11-2704922
      Fax: +55-11-2707001
      Email: asimpson@ludwig.org.br
      This sequence was derived from the FAPESP/LICR Human Cancer Genome
      project. This entry can be seen in the following URL
      (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-MRI-BT0796-160
      600-001-c10&ts=2000-06-16&td=1)
      Seq primer: puc 18 forward
      High quality sequence start: 13
      High quality sequence stop: 100.
FEATURES
      source
      1..100
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      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone_lib="BT0796"
      /dev_stage="Adult"
      /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
      SmaI; A mini-library was made by cloning products derived
      from ORESTES PCR (U.S. Letters Patent application No. 196
      ,716 - Ludwig Institute for Cancer Research) profiles
      into the pUC 18 vector. Reverse transcription of tissue
      mRNA and cDNA amplification were performed under low
      stringency conditions."

BASE COUNT      24 a      30 c      23 g      23 t
ORIGIN

Query Match      1.1%; Score 58; DB 12; Length 100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1226 GGTCTGGCCTATGACCGGAGAAAGTCTCCAGGCCGCCATCTTGCCACGATTAAAA 1283
      |||
Db   43 GGTCTGGCCTATGACCGGAGAAAGTCTCCAGGCCGCCATCTTGCCACGATTAAAA 100

RESULT 4
A0103573
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LOCUS AU103573 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU103573 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP13102, mRNA sequence.
ACCESSION AU103573
VERSION AU103573.1 GI:13553094
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
TITLE
JOURNAL
MEDLINE
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
source
1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP13102"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumurate treated U937 cells"
BASE COUNT 8 a 18 c 12 g 12 t
ORIGIN
Query Match 1.0%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 ACCGTCACCCGTGCGACCTCTAGCCTTAATTCCTCCGGCTCGGGACCT 78
|||||
Db 1 ACCGTCACCCGTGCGACCTCTAGCCTTAATTCCTCCGGCTCGGGACCT 50
RESULT 5
AU103578 50 bp mRNA linear EST 30-AUG-2001
LOCUS AU103578 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADSE01417, mRNA sequence.
ACCESSION AU103578
VERSION AU103578.1 GI:13553099
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
TITLE
JOURNAL
MEDLINE
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
source
1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADSE01417"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumurate treated U937 cells"
BASE COUNT 10 a 19 c 17 g 4 t
ORIGIN
Query Match 1.0%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 85 ACCGCGCTAGCGCCGACACCACTAGCTGCAAGCGCGCGCTCAG 134
|||||
Db 1 ACCGCGCTAGCGCCGACACCACTAGCTGCAAGCGCGCGCTCAG 50
RESULT 6
AU103571 50 bp mRNA linear EST 30-AUG-2001
LOCUS AU103571 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP07904, mRNA sequence.
ACCESSION AU103571
VERSION AU103571.1 GI:13553092
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
TITLE
JOURNAL
MEDLINE
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
source
1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP07904"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumurate treated U937 cells"
BASE COUNT 9 a 19 c 17 g 5 t
ORIGIN
Query Match 0.9%; Score 47; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 GCACCGCGGCTAGCGCGACACCACTAGCGTGCAAGCGCGCGG 129
|||||
Db 1 GCACCGCGGCTAGCGCGACACCACTAGCGTGCAAGCGCGCGG 47
RESULT 7
BG255827 74 bp mRNA linear EST 13-FEB-2001
LOCUS BG255827
DEFINITION 602368138P1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4476417 5',

MRNA sequence.
ACCESSION BG255827 GI:12765643
VERSION BG255827.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 74)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Plate: L1AM10303 row: k column: 10
High quality sequence stop: 41.
Location/Qualifiers
1. 74
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4476417"
/clone_1lb="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; Oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."
BASE COUNT 11 a 14 c 24 g 25 t
ORIGIN
Query Match 0.8%; Score 43; DB 12; Length 74;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2283 CCATCTTCAGGATATGTTCTTCCCTCATAGTATAGATG 2325
Db 1 CCATCTTCAGGATATGTTCTTCCCTCATAGTATAGATG 43
RESULT 8
LOCUS BI223563 42 bp mRNA linear EST 11-JUL-2001
DEFINITION 602941991F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5104919 5', mRNA sequence.
ACCESSION BI223563
VERSION BI223563.1 GI:14677007
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 42)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Plate: L1AM11253 row: f column: 24
High quality sequence stop: 42.
Location/Qualifiers
1. 42
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5104919"
/clone_1lb="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."
BASE COUNT 10 a 11 c 12 g 9 t
ORIGIN
Query Match 0.8%; Score 42; DB 13; Length 42;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3294 AGAACGAGGCGATGCTGAATGCCCTGCTTACTTGGA 3335
Db 1 AGAACGAGGCGATGCTGAATGCCCTGCTTACTTGGA 42
RESULT 9
LOCUS AA501922 68 bp mRNA linear EST 18-AUG-1997
DEFINITION ng54d08.s1 NCI_CGAP_L12 Homo sapiens CDNA clone IMAGE:938607, mRNA sequence.
ACCESSION AA501922
VERSION AA501922.1 GI:2236889
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 68)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David E. Kleiner, M.D., Ph.D., Ph.D.
Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 607 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 51.
Location/Qualifiers
1. 68
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/clone="IMAGE:938607"
/clone_1lb="NCI_CGAP_L12"
/sex="male"
/tissue_type="liver"
/lab_host="DH10B"
/note="Vector: pAMP10; mRNA made from invasive hepatocellular carcinoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
BASE COUNT 12 a 20 c 17 g 19 t
ORIGIN

Query Match 0.8%; Score 40; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2972 AGTGATGACTGCTGCTCCAGCAGCTCCCTCCTGCACACA 3011
|||||
Db 29 AGTGATGACTGCTGCTCCAGCAGCTCCCTCCTGCACACA 68

RESULT 10
BI259338 32 bp mRNA linear EST 17-JUL-2001
LOCUS 602972590F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5111783 5',
DEFINITION mRNA sequence.
ACCESSION BI259338
VERSION BI259338.1 GI:14816575
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 32)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1A11271 row: d column: 24
High quality sequence stop: 32.
Location/Qualifiers

FEATURES
source 1..32
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5111783"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

BASE COUNT 5 a 9 c 9 g 9 t
ORIGIN

Query Match 0.6%; Score 32; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3304 GGCATGCTGAATGCCCTGCTTACTTGTTGA 3335
|||||
Db 1 GGCATGCTGAATGCCCTGCTTACTTGTTGA 32

RESULT 11
AUI03576 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI03576 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP21416, mRNA sequence.
ACCESSION AUI03576
VERSION AUI03576.1 GI:13553097
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)

AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP21416"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"

BASE COUNT 11 a 11 c 19 g 9 t
ORIGIN

Query Match 0.5%; Score 28; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 AGCCTTTAAATTCCTCGGCTCGGGACCT 78
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Db 1 AGCCTTTAAATTCCTCGGCTCGGGACCT 28

RESULT 12
AUI03570 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI03570 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP02242, mRNA sequence.
ACCESSION AUI03570
VERSION AUI03570.1 GI:13553091
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP02242"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"

BASE COUNT 11 a 11 c 19 g 9 t
ORIGIN

Query Match 0.5%; Score 26; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAAAGGGGCTGAGGAATACCGG 26
|||||
Db 25 ATAAAGGGGCTGAGGAATACCGG 50

RESULT 13
AU103572 50 bp mRNA linear EST 30-AUG-2001
LOCUS AU103572 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP12765, mRNA sequence.
ACCESSION AU103572
VERSION AU103572.1 GI:13553093
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
TITLE Contact: Yutaka Suzuki
JOURNAL Department of Virology
MEDLINE Institute of Medical Science, University of Tokyo
COMMENT 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP12765"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"

BASE COUNT 8 a 16 c 12 g 14 t
ORIGIN

Query Match 0.5%; Score 24; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ACGGTCAACCGTTGCCAGCTCTAG 52
|||||
Db 1 ACGGTCAACCGTTGCCAGCTCTAG 24

RESULT 14
AA544229 92 bp mRNA linear EST 01-AUG-1997
LOCUS AA544229 vj63d12.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA
DEFINITION clone IMAGE:933719 5' similar to gb:S74678 HETEROGENEOUS NUCLEAR
RIBONUCLEOPROTEIN K (HUMAN);, mRNA sequence.
ACCESSION AA544229
VERSION AA544229.1 GI:2292706
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 92)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

TITLE
JOURNAL
COMMENT
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:538639.

FEATURES
source
1..92
/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:933719"
/clone_lib="Knowles Solter mouse blastocyst B1"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pSPORT; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally from mRNA prepared
from 800 blastocysts. Primer: SalI(dT):
5'-CGGTCGACCGTCGACCGTTTCTTTT-3'. cDNAs were
cloned into the NotI/SalI sites of a pSPORT vector (Life
Technologies). Two different size selections: B1 (larger
inserts) and B3."

BASE COUNT 51 a 5 c 10 g 26 t
ORIGIN

Query Match 0.5%; Score 24; DB 9; Length 92;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5198 AGTGAATCTAAAAA 5221
|||||
Db 55 AGTGAATCTAAAAA 78

RESULT 15
BE957444 68 bp mRNA linear EST 14-DEC-2000
LOCUS BE957444 601653588R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838701 3',
DEFINITION mRNA sequence.
ACCESSION BE957444
VERSION BE957444.2 GI:11773914
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 68)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Oct 3, 2000 this sequence version replaced gi:10568253.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM525 row: O column: 22
High quality sequence stop: 52.

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2002, 01:13:16 ; Search time 8670 seconds
(without alignments)
17525.461 Million cell updates/sec

Title: US-09-918-187-3
Perfect score: 5221
Sequence: 1 ataaaggggggtgaggaaa.....aatctaaaaaaaaaaaaaa 5221

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 993650

Minimum DB seq length: 8
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	39	0.7	39	6	AR003340	AR003340 Sequence
2	21	0.4	95	6	AR002350	AR002350 Sequence
3	21	0.4	95	6	AR030853	AR030853 Sequence
4	21	0.4	95	6	AR068248	AR068248 Sequence
5	21	0.4	95	6	186799	186799 Sequence 3
6	20	0.4	25	6	AX043282	AX043282 Sequence
7	20	0.4	91	3	DDIACFINBA	M25215 Dictyosteli
8	20	0.4	94	11	G73641	G73641 R2696F etlo
9	19	0.4	28	6	AX431447	AX431447 Sequence
10	19	0.4	65	6	AX484032	AX484032 Sequence
11	18	0.3	18	6	E32451	E32451 Mammal-deri
12	18	0.3	35	6	AR051300	AR051300 Sequence
13	18	0.3	35	6	116948	116948 Sequence 17
14	18	0.3	35	6	145742	145742 Sequence 17
15	18	0.3	42	6	AR184440	AR184440 Sequence
16	18	0.3	42	6	AX354550	AX354550 Sequence
17	18	0.3	42	6	AX428578	AX428578 Sequence
18	18	0.3	45	6	AX235169	AX235169 Sequence
19	18	0.3	46	6	AX287576	AX287576 Sequence
20	18	0.3	46	6	AX287580	AX287580 Sequence
21	18	0.3	51	6	AX158375	AX158375 Sequence
22	18	0.3	51	6	AX158377	AX158377 Sequence
23	18	0.3	51	6	AX398977	AX398977 Sequence
24	18	0.3	51	6	AX398978	AX398978 Sequence
25	18	0.3	62	6	A12493	A12493 polYadenyla
26	18	0.3	65	6	AX485279	AX485279 Sequence
27	18	0.3	71	3	AF177248	AF177248 Bodo salt
28	18	0.3	72	6	AX381283	AX381283 Sequence
29	18	0.3	72	6	AX381405	AX381405 Sequence
30	18	0.3	74	6	AX203346	AX203346 Sequence
31	18	0.3	74	6	AX381324	AX381324 Sequence
32	18	0.3	74	6	AX381456	AX381456 Sequence
33	18	0.3	79	6	AX381268	AX381268 Sequence
34	18	0.3	81	6	AX381811	AX381811 Sequence
35	18	0.3	83	10	MMARK007	X58263 Mouse micro
36	18	0.3	89	9	HUMPODAT02	D17700 Human gene
37	18	0.3	90	6	AX198863	AX198863 Sequence
38	18	0.3	90	6	AX209390	AX209390 Sequence
39	18	0.3	90	6	AX381219	AX381219 Sequence
40	18	0.3	90	6	AX381279	AX381279 Sequence
41	18	0.3	97	6	AX260590	AX260590 Sequence
42	18	0.3	98	6	AX198479	AX198479 Sequence
43	18	0.3	98	6	AX209025	AX209025 Sequence
44	17	0.3	17	6	BD011732	BD011732 795, a no
45	17	0.3	17	6	E34260	E34260 Pollinosis-

ALIGNMENTS

RESULT 1
AR003340
LOCUS AR003340 39 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 62 from patent US 5744300.
ACCESSION AR003340
VERSION AR003340.1 GI:3964599
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 39)
AUTHORS Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
West,M.David.
TITILE Methods and reagents for the identification and regulation of
senescence-related genes

JOURNAL Patent: US 5744300-A 62 28-APR-1998;
FEATURES Location/Qualifiers

source 1..39

BASE COUNT 11 a 7 c 6 g 15 t
ORIGIN

Query Match 0.7%; Score 39; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 AGATGATGATGTTAACCACATTCACAGTATCTTTT 1450

Db 1 AGATGATGATGTTAACCACATTCACAGTATCTTTT 39

RESULT 2
AR002350 LOCUS AR002350 95 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 3 from patent US 5741666.
ACCESSION AR002350
VERSION AR002350.1 GI:3963904
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 95)
AUTHORS Tartaglia,L.Anthony.
TITLE Compositions and methods, for the treatment of body weight disorders, including obesity
JOURNAL Patent: US 5741666-A 3 21-APR-1998;
FEATURES Location/Qualifiers
source 1..95

BASE COUNT 24 a 24 c 16 g 31 t
ORIGIN

Query Match 0.4%; Score 21; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089
Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 3
AR030853 LOCUS AR030853 95 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5861485.
ACCESSION AR030853
VERSION AR030853.1 GI:5944067
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 95)
AUTHORS Tartaglia,L.Anthony.
TITLE Polypeptides involved in body weight disorders, including obesity
JOURNAL Patent: US 5861485-A 3 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..95

BASE COUNT 24 a 24 c 16 g 31 t
ORIGIN

Query Match 0.4%; Score 21; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089
Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 4
AR068248 LOCUS AR068248 95 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5853975.
ACCESSION AR068248
VERSION AR068248.1 GI:6000455
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 95)
AUTHORS Tartaglia,L.Anthony.
TITLE Methods for identifying compositions for the treatment of body weight disorders, including obesity
JOURNAL Patent: US 5853975-A 3 29-DEC-1998;
FEATURES Location/Qualifiers
source 1..95

BASE COUNT 24 a 24 c 16 g 31 t
ORIGIN

Query Match 0.4%; Score 21; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089
Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 5
I86799 LOCUS I86799 95 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 3 from patent US 5702902.
ACCESSION I86799
VERSION I86799.1 GI:3206517
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 95)
AUTHORS Tartaglia,L.Anthony.
TITLE Methods for the diagnosis of body weight disorders including obesity
JOURNAL Patent: US 5702902-A 3 30-DEC-1997;
FEATURES Location/Qualifiers
source 1..95

BASE COUNT 24 a 24 c 16 g 31 t
ORIGIN

Query Match 0.4%; Score 21; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089
Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 6
AX043282 LOCUS AX043282 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 848 from Patent WO0065088.
ACCESSION AX043282
VERSION AX043282.1 GI:11341890
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 25)

REFERENCE 1 (bases 1 to 25)

Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4498 AAGTTT TTTT TTTT TT 4515

Db 16 AAGTTT TTTT TTTT TT 33

RESULT 14

I45742

LOCUS I45742 35 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 17 from patent US 5637685.

ACCESSION I45742

VERSION I45742.1 GI:2469844

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

1 (bases 1 to 35)

AUTHORS Soares, M.B. and Efstratiadis, A.

TITLE Normalized cDNA libraries

JOURNAL Patent: US 5637685-A 17 10-JUN-1997;

FEATURES Location/Qualifiers

source 1..35

BASE COUNT 7 a 0 c 1 g 27 t

ORIGIN

Query Match 0.3%; Score 18; DB 6; Length 35;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4498 AAGTTT TTTT TTTT TT 4515

Db 16 AAGTTT TTTT TTTT TT 33

RESULT 15

AR184440/c

LOCUS AR184440 42 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 8 from patent US 6346384.

ACCESSION AR184440

VERSION AR184440.1 GI:20230405

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

1 (bases 1 to 42)

AUTHORS Pollner, R.B.

-TITLE Real-time monitoring of PCR using LOCI

JOURNAL Patent: US 6346384-A 8 12-FEB-2002;

FEATURES Location/Qualifiers

source 1..42

BASE COUNT 4 a 6 c 4 g 28 t

ORIGIN

Query Match 0.3%; Score 18; DB 6; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5204 TCTAAAAA AAAAAA AAAAAA 5221

Db 23 TCTAAAAA AAAAAA AAAAAA 6

Search completed: November 14, 2002, 05:50:56
Job time : 8697 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 13, 2002, 18:48:56 ; Search time 115 seconds
(without alignments)
13923.125 Million cell updates/sec

Title: US-09-918-187-3
Perfect score: 5221
Sequence: 1 atataaagggggctgagga...aatctataaaaaaaaaaaaaa 5221

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 684418

Minimum DB seq length: 8
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Issued Patents_NA:
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2: /cgcn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgcn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgcn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgcn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgcn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	0.7	39	1	US-08-332-420-62
2	21	0.4	95	1	US-08-518-878B-3
3	21	0.4	95	1	US-08-294-522B-3
4	21	0.4	95	2	US-08-807-861A-3
5	21	0.4	95	2	US-08-470-868A-3
6	21	0.4	95	3	US-09-210-681-3
7	21	0.4	95	3	US-08-946-719A-3
8	18	0.3	23	5	PCT-US94-05407-7
9	18	0.3	23	5	PCT-US94-05407-8
10	18	0.3	33	3	US-09-187-355-1
11	18	0.3	35	1	US-08-126-594-17
12	18	0.3	35	1	US-08-465-811A-17
13	18	0.3	35	2	US-08-619-542B-17
14	18	0.3	38	2	US-08-771-624B-21
15	18	0.3	39	4	US-09-619-103-4
16	18	0.3	42	4	US-09-536-936-8
17	18	0.3	46	1	US-07-915-245-3
18	18	0.3	46	5	PCT-US94-05407-3
19	18	0.3	46	5	PCT-US94-05407-10
20	18	0.3	68	3	US-09-052-924-1
21	17	0.3	20	1	US-07-912-900-20
22	17	0.3	20	1	US-08-853-309-20
23	17	0.3	20	1	US-08-313-075A-11
24	17	0.3	20	2	US-08-502-046-20
25	17	0.3	20	3	US-09-120-853-4
26	17	0.3	20	4	US-09-228-942-7
27	17	0.3	20	4	US-08-482-918-32

c 28	17	0.3	20	4	US-08-482-918-33	Sequence 33, Appl
c 29	17	0.3	20	4	US-09-224-681-32	Sequence 32, Appl
c 30	17	0.3	20	4	US-09-224-681-33	Sequence 33, Appl
c 31	17	0.3	20	4	US-08-336-728A-32	Sequence 32, Appl
c 32	17	0.3	20	4	US-08-336-728A-33	Sequence 33, Appl
c 33	17	0.3	23	1	US-08-018-129-15	Sequence 15, Appl
c 34	17	0.3	23	1	US-08-621-914A-6	Sequence 6, Appl
c 35	17	0.3	23	2	US-08-448-250-15	Sequence 15, Appl
c 36	17	0.3	23	3	US-09-056-052-9	Sequence 9, Appl
c 37	17	0.3	24	4	US-08-906-156A-82	Sequence 82, Appl
c 38	17	0.3	26	1	US-08-014-943A-21	Sequence 21, Appl
c 39	17	0.3	26	1	US-08-486-421-15	Sequence 15, Appl
c 40	17	0.3	26	1	US-08-470-911-15	Sequence 15, Appl
c 41	17	0.3	26	2	US-08-486-809-15	Sequence 15, Appl
c 42	17	0.3	26	4	US-09-475-316A-59	Sequence 59, Appl
c 43	17	0.3	30	1	US-08-181-271A-85	Sequence 85, Appl
c 44	17	0.3	30	1	US-08-158-189-43	Sequence 43, Appl
c 45	17	0.3	30	1	US-08-449-315-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-08-332-420-62
Sequence 62, Application US/08332420
Patent No. 5744300
GENERAL INFORMATION:
APPLICANT: Maarten H.K. Linskens, et al.
TITLE OF INVENTION: METHODS AND REAGENTS FOR THE
TITLE OF INVENTION: IDENTIFICATION AND REGULATION
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,420
FILING DATE: October 31, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/235,180
FILING DATE: April 29, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 39
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-332-420-62

Query Match 0.7%; Score 39; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1412 AGATGATGATGTTAACCATTTCAGTACAGTATCTTTT 1450

Db 1 AGATGATGATGTTAACCATTCACAGTATCTTTT 39

RESULT 2

US-08-518-878B-3

; Sequence 3, Application US/08518878B

; Patent No. 5702902

; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/518,878B

; FILING DATE: 23-AUG-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7853-036

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 95 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-518-878B-3

Query Match 0.4%; Score 21; DB 1; Length 95;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089

Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 3

US-08-294-522B-3

; Sequence 3, Application US/08294522B

; Patent No. 5741666

; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.

; TITLE OF INVENTION: Compositions and Methods for the

; TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/294,522B

; FILING DATE: 23-AUG-1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7853-015

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-8864/9741

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 95 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; US-08-294-522B-3

Query Match 0.4%; Score 21; DB 1; Length 95;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089

Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 4

US-08-807-861A-3

; Sequence 3, Application US/08807861A

; Patent No. 5853975

; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE

; TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/807,861A

; FILING DATE: 26-FEB-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/518,878

; FILING DATE: 23-AUG-1995

; APPLICATION NUMBER: US 08/470,868

; FILING DATE: 06-JUN-1995

; APPLICATION NUMBER: US 08/294,522

; FILING DATE: 23-AUG-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7853-066

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 95 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-807-861A-3

Query Match 0.4%; Score 21; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089
|||||
DB 74 TTTTTCCTTTTATGTGGG 94

RESULT 5
US-08-470-868A-3

Sequence 3, Application US/08470868A
Patent No. 5861485

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis C.

TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders, including Obesity

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie and Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,868A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-0031-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

TELEX: 66441 PENNIE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 95 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-470-868A-3

Query Match 0.4%; Score 21; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089
|||||
DB 74 TTTTTCCTTTTATGTGGG 94

RESULT 6
US-09-210-681-3

Sequence 3, Application US/09210681

Patent No. 6057109

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE

TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/210,681

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/807,861

FILING DATE: 26-FEB-1997

APPLICATION NUMBER: US 08/518,878

FILING DATE: 23-AUG-1995

APPLICATION NUMBER: US 08/470,868

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/294,522

FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-066

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 95 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-210-681-3

Query Match 0.4%; Score 21; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089
|||||
DB 74 TTTTTCCTTTTATGTGGG 94

RESULT 7.
US-08-946-719A-3

Sequence 3, Application US/08946719A

Patent No. 6121017

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

```

: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/946,719A
: FILING DATE: 8-OCT-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/807,861
: FILING DATE: 26-FEB-1997
: APPLICATION NUMBER: US 08/518,878
: FILING DATE: 23-AUG-1995
: APPLICATION NUMBER: US 08/470,868
: FILING DATE: 06-JUN-1995
: APPLICATION NUMBER: US 08/294,522
: FILING DATE: 23-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7853-107
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 95 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-946-719A-3

Query Match          0.4%; Score 21; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089
Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 8
PCT-US94-05407-7/C
: Sequence 7, Application PC/TUS9405407
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NEEDLE & ROSENBERG, P.C.
: STREET: Suite 1200, 127 Peachtree Street
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30303
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/05407
: PRIOR APPLICATION NUMBER: 08/061,694
: FILING DATE: 13-MAY-1993
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 23 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: oligonucleotide
PCT-US94-05407-7

Query Match          0.3%; Score 18; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4501 TTTTTCCTTTTATGTGGG 4518
Db 20 TTTTTCCTTTTATGTGGG 3

RESULT 9
PCT-US94-05407-8
: Sequence 8, Application PC/TUS9405407
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NEEDLE & ROSENBERG, P.C.
: STREET: Suite 1200, 127 Peachtree Street
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30303
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/05407
: PRIOR APPLICATION NUMBER: 08/061,694
: FILING DATE: 13-MAY-1993
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 23 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: oligonucleotide
PCT-US94-05407-8

Query Match          0.3%; Score 18; DB 5; Length 23;
Best Local Similarity 16.7%; Pred. No. 7.8e+02;
Matches 3; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

QY 4501 TTTTTCCTTTTATGTGGG 4518
Db 4 UUUUUUUUUUUUUUUUUUUUU 21

RESULT 10
US-09-187-355-1
: Sequence 1, Application US/09187355B
: Patent No. 618126
: GENERAL INFORMATION:
: APPLICANT: Sarnoff Corporation
: APPLICANT: Zanzucchi, Peter F.
: TITLE OF INVENTION: Method for Enhancing Fluorescence
: FILE REFERENCE: SAR-12215A
: CURRENT APPLICATION NUMBER: US/09/187,355B
: CURRENT FILING DATE: 1998-11-06
: EARLIER APPLICATION NUMBER: US 08/961,860
: EARLIER FILING DATE: 1997-10-31
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 33
: TYPE: DNA
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Unknown Organism
US-09-187-355-1

Query Match          0.3%; Score 18; DB 3; Length 33;
```

Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4498 AAGTTTTTTTTTTTTT 4515
|||||
Db 15 AAGTTTTTTTTTTTTT 32

RESULT 11

US-08-126-594-17
; Sequence 17, Application US/08126594
; Patent No. 5482845
; GENERAL INFORMATION:
; APPLICANT: Soares, M. Bento
; APPLICANT: Efstathiadis, Algitis
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
; TITLE OF INVENTION: CDNA LIBRARIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, c/o Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/126,594
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-126-594-17

Query Match 0.3%; Score 18; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4498 AAGTTTTTTTTTTTTT 4515
|||||
Db 16 AAGTTTTTTTTTTTTT 33

RESULT 12

US-08-465-811A-17
; Sequence 17, Application US/08465811A
; Patent No. 5637685
; GENERAL INFORMATION:
; APPLICANT: Soares, M. Bento
; APPLICANT: Efstathiadis, Algitis
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
; TITLE OF INVENTION: NORMALIZED CDNA LIBRARIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White, c/o Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,811A
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-465-811A-17

Query Match 0.3%; Score 18; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4498 AAGTTTTTTTTTTTTT 4515
|||||
Db 16 AAGTTTTTTTTTTTTT 33

RESULT 13

US-08-619-542B-17
; Sequence 17, Application US/08619542B
; Patent No. 5830662
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City
; APPLICANT: of New York
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
; TITLE OF INVENTION: CDNA LIBRARIES
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/619,542B
; FILING DATE: June 21, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42840-A-PCT-US

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-619-542B-17

Query Match          0.3%; Score 18; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4498 AGCTTTT TTTT TTTT TTTT 4515
Db 16 AAGTTT TTTT TTTT TTTT 33

RESULT 14
US-08-771-624B-21
; Sequence 21, Application US/08771624B
; Patent No. 5914230
; GENERAL INFORMATION:
; APPLICANT: Liu, Yen Ping
; APPLICANT: Patel, Rajesh D.
; APPLICANT: Kurn, Nurith
; APPLICANT: Lin, Claire
; APPLICANT: Rose, Samuel J.
; APPLICANT: Ullman, Edwin F.
; TITLE OF INVENTION: Homogeneous Amplification and Detection
; TITLE OF INVENTION: of Nucleic Acids
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Behring Diagnostics GmbH, c/o Dade Behring Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: US
; ZIP: 60015-0778
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/771,624B
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/009,090
; FILING DATE: 22-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ruzsala, Lois K.
; REGISTRATION NUMBER: 39,074
; REFERENCE/DOCKET NUMBER: 1030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 267-5364
; TELEFAX: (847) 267-6024
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
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; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
US-08-771-624B-21

Query Match          0.3%; Score 18; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4498 AGCTTTT TTTT TTTT TTTT 4515
Db 16 AAGTTT TTTT TTTT TTTT 33

RESULT 15
US-09-619-103-4
; Sequence 4, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence to act as a linker
US-09-619-103-4

Query Match          0.3%; Score 18; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5204 TCTA A A A A A A A A A A A A A A 5221
Db 8 TCTA A A A A A A A A A A A A A A 25
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Search completed: November 14, 2002, 01:16:48
Job time : 119 secs